



STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/520,033
Source: PCR/10
Date Processed by STIC: 1/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/520,033

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 J Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/520,033

DATE: 01/10/2006

TIME: 08:16:21

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

see item 2 on Encl summary sheet

3 <110> APPLICANT: Chan, Raquel
 5 <120> TITLE OF INVENTION: Transcription factor gene induced by water deficit conditions and
 6 abscisic acid from Helianthus annuus, promoter and transgenic plants
 8 <130> FILE REFERENCE: US PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/520,033
 C--> 10 <141> CURRENT FILING DATE: 2004-12-30
 10 <160> NUMBER OF SEQ ID NOS: 22
 12 <170> SOFTWARE: PatentIn version 3.1

these lines exceed 72 character

see pp 1-6

ERRORED SEQUENCES

E--> 14 <210> ~~SEQ ID NO. 1~~ *delete all alphabetical headings 1 - just show "1"*
 15 <211> LENGTH: 774
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Helianthus annuus
 OK-> 19 <400> SEQUENCE: 1

**Does Not Comply
Corrected Diskette Needed**

do NOT use alphabetical heading in a "new" sequence
rules format sequence listing

20 tcactagtagc cataatatcc acaaacacac acacctcaga aacgaagctt gcacataatg 60
 22 tctcttcaac aagtaccac aacagaaaca accaccagga agaaccgaaa cgagggcgcg 120
 24 aaacgattta cgcacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga 180
 26 cccgagttta ggatgaaaca ccagttggca cataaactcg ggcttcaccc tegtcaagt 240
 28 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat 300
 30 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtcctt aaagaaagag 360
 32 aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcat caactattta 420
 34 agtagttttg aatttttgtg acaataaaga ttgacaaatg ttgtttgata attgattaac 480
 36 agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtgga 540
 38 gcggtgaaga atcgatgat cggtttacga actctccgga cgttatggtt ggtcaagaaa 600
 40 tgaatgttcc gttttgcgac ggttttgctt actttgaaga aggaaacagt ttgttgagaa 660
 42 ttgaagaaca actgccagac cctcaaaagt ggtgggagtt cttaaagagta aagaaggatg 720
 44 tagaagtagt agagtaaaaa ctaaaacata ccagatagtt ggtttacact ttgt 774

E--> 47 <210> ~~SEQ ID NO. 2~~
 48 <211> LENGTH: 673
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Helianthus annuus

OK-> 52 <400> SEQUENCE: 2
 53 tcactagtagc cataatatcc acaaacacac acacctcaga aacgaagctt gcacataatg 60
 55 tctcttcaac aagtaccac aacagaaaca accaccagga agaaccgaaa cgagggcgcg 120
 57 aaacgattta cgcacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga 180
 59 cccgagttta ggatgaaaca ccagttggca cataaactcg ggcttcaccc tegtcaagt 240
 61 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat 300
 63 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtcctt aaagaaagag 360
 65 aatcaggccc tactcaatca gttggaggtg ctgagaaatg tagcagaaaa gcatcaagag 420
 67 aaaactagta gtagtggcag cggatgaaga tcggatgatc gggtttacgaa ctctccggac 480

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Input Set : A:\PTO.DA.txt

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```

69 gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa 540
71 ggaaacagtt tggtggagat tgaagaacaa ctgccagacc ctcaaaagtgt gtgggagttc 600
73 taaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagtgt 660
75 gtttacactt tgt 673

```

E--> 78 <210> ~~SEQ ID NO. 3~~

```

79 <211> LENGTH: 1221
80 <212> TYPE: DNA
81 <213> ORGANISM: Helianthus annuus
83 <220> FEATURE:
84 <221> NAME/KEY: promoter
85 <222> LOCATION: (1)..(1221)
86 <223> OTHER INFORMATION: Large allele

```

E--> 89 <400> SEQUENCE: 3

```

90 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca 60
92 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc 120
94 atattaaaag tagtagcccc caccgccatt tgttacctac catttcccac ttttaataatc 180
96 acccagccta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa 240
98 ccaaattttt tttagtggaa aacaaattcc ccaaatagaa tactaacgaa attcatcgca 300
100 tcagaatata ctcactctctg aacagtggcg aagcttgacg ttttcgacgg ggggtcgga 360
102 aacgtatgta cccgaaattt ctatagaatc ggggggtcga aaacgtatat acccaaaatt 420
104 tctatacgaa aactacatat ataacactac tgagcaaaaa gttcgggggt tcgggcgccc 480
106 ctcccgcccc cttcaaagct tcgccaatgt ctctgaaccg aagaaaaccc tcactcgtct 540
108 actagccaat gaatcctcac cagggaacc ctcactcgtc ttactggact attggcgctt 600
110 ccaaattggac tacttgcgaa attcaccaca tcgggataca ctcgtctact gcggtgaggt 660
112 aaaacccgct tggctcaagg atcgaaactag cgattgctgc ctactcgcct aatctcccat 720
114 catcaacagg tgccgcccga acaaaatgct gggggcgga gttgaacctt ggtccagtga 780
116 cgcacccatg aatttttttt ctagggatgc gaacgagtgg ttttaaccata cttttaagag 840
118 gtgcgatcgg aaattttacc tataaaatac actaaaaaag ttccaagggt ccaccaccc 900
120 cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggctctct ccttaccagt 960
122 ccagctacga ctattgaca aaatatcaaa accatatgat tttgagtttt atctcaaccg 1020
124 aaagtgcacat catgcacagag aatcgacata accaaaacgt gtaaaccgtac aactcaccat 1080
126 tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct 1140
128 tcatctaaac ccatacttt aagaaccttt ataaagacca ctactatat atacacatat 1200
130 ataatatcac ttatcaaacc c 1221

```

E--> 133 <210> ~~SEQ ID NO. 4~~

```

134 <211> LENGTH: 28
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having

```

Hind I

140 II site

E--> 142 <400> SEQUENCE: 4

```

143 gcgaagcttg atgcgaacga gtggttta 28

```

E--> 146 <210> ~~SEQ ID NO. 5~~

```

147 <211> LENGTH: 28
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having

```

Sal I

RAW SEQUENCE LISTING

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

153 site
 155 <400> SEQUENCE: 5
 156 gcggtcgaca cctggcacat cgtatctt 28
 E--> 159 <210> : ~~SEQ ID NO. 6~~
 160 <211> LENGTH: 27
 161 <212> TYPE: DNA
 162 <213> ORGANISM: Artificial
 164 <220> FEATURE:
 165 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Bam HI
 166 site
 168 <400> SEQUENCE: 6
 169 cgcggatccg agggtttgat aagtgat 27
 E--> 172 <210> ~~SEQ ID NO. 7~~
 173 <211> LENGTH: 27
 174 <212> TYPE: DNA
 175 <213> ORGANISM: Artificial
 177 <220> FEATURE:
 178 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Hind I
 179 II site
 181 <400> SEQUENCE: 7
 182 cccaagctta acctaagtcc gcctttg 27
 E--> 185 <210> ~~SEQ ID NO. 8~~
 186 <211> LENGTH: 27
 187 <212> TYPE: DNA
 188 <213> ORGANISM: Artificial
 190 <220> FEATURE:
 191 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
 Hind II
 192 I site
 194 <400> SEQUENCE: 8
 195 ggcaagctta tctcaaccga aagtgc 27
 E--> 198 <210> ~~SEQ ID NO. 9~~
 199 <211> LENGTH: 19
 200 <212> TYPE: DNA
 201 <213> ORGANISM: Artificial
 203 <220> FEATURE:
 204 <223> OTHER INFORMATION: Designed oligonucleotide based on the 5' promoter
 206 <400> SEQUENCE: 9
 207 atttcgcaag tagtcatt 19
 E--> 210 <210> ~~SEQ ID NO. 10~~
 211 <211> LENGTH: 1015
 212 <212> TYPE: DNA
 213 <213> ORGANISM: Helianthus annuus
 215 <400> SEQUENCE: 10
 216 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca 60
 218 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc 120
 220 atattaaaag tagtagcccc cccccccatt tgttacctac catttcccac ttttaataatc 180
 222 acccacgcta tgtccacttg tacttttgggt tgcacacaac tcttcccata aaatatcaaa 240
 224 ccaaattttt tttaaatggaa aacaaatact tcaaatagcac tattgggtgaa attcaccaca 300
 226 tcagaatata cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc 360

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

```

228 actcgtctac tgggactact ggcgcttcaa aatggactac tgacaaaatt caccacatcg 420
230 ggatacactt gtctactgcg gtgaggtaaa atccgccgct cagctcaatg atcgaactag 480
232 cgatcgccac ccactcacct tgtctcccat catcaccagg tgccgccaaa acaaaatgtt 540
234 gggggcgggg attgaacctt ggtccagtgg cgcacccatg aatttttttt ctagggatgc 600
236 gaacgagtga ttttaaccata cttttaagag gtgcgatcgg aaattttacc tataaaatat 660
238 actaaaaaaaa tttcaagggt cgcgccacc accccttaac ctaagtccgc ctctgcctgg 720
240 atcacgtgaa acatcagggtc tctctcttac cagttcacct acaactcatt gacaaaatat 780
242 caaaaccata tgattttgag ttttatctca accgaaagtg acatcatgac agagaatcga 840
244 cataacccaaa acgtgtaaac gtacaactca ccattgcgtt gaaaaggaca aaacaggtag 900
246 gattcttgct aaattcaacg cgtacacctg tgcttcatct aaacccata ctttaagaac 960
248 ctttataaag accactcact atatatacac atatataata tcacttatca aacctt 1015

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E--> 251 <210> ~~SEQ ID NO. 11~~

252 <211> LENGTH: 28

253 <212> TYPE: DNA

254 <213> ORGANISM: Artificial

256 <220> FEATURE:

257 <223> OTHER INFORMATION: Designed oligonucleotide that matches nucleotides 81-100 of the H

258 ahb-4 cDNA sequence and having Bam HI site

E--> 260 <400> ~~SEQUENCE: 11~~

261 ggcggatcca acagaaacaa ccaccagg 28

E--> 264 <210> ~~SEQ ID NO. 12~~

265 <211> LENGTH: 29

266 <212> TYPE: DNA

267 <213> ORGANISM: Artificial

269 <220> FEATURE:

270 <223> OTHER INFORMATION: Designed oligonucleotide for cloning 5' cDNA and having Bam HI s

271 ite

E--> 273 <400> ~~SEQUENCE: 12~~

274 ggcggatccc ctggtggttg tttctgttg 29

E--> 277 <210> ~~SEQ ID NO. 13~~

278 <211> LENGTH: 34

279 <212> TYPE: DNA

280 <213> ORGANISM: Artificial

282 <220> FEATURE:

283 <223> OTHER INFORMATION: oligonucleotide based on 5' cDNA and having Xho I site

E--> 285 <400> ~~SEQUENCE: 13~~

286 gaggactcga gctcaagttt tttttttttt tttt 34

E--> 289 <210> ~~SEQ ID NO. 14~~

290 <211> LENGTH: 18

291 <212> TYPE: DNA

292 <213> ORGANISM: Artificial

294 <220> FEATURE:

295 <223> OTHER INFORMATION: Oligonucleotide based on 5' cDNA and having Xho I site

E--> 297 <400> ~~SEQUENCE: 14~~

298 gaggactcga gctcaagc 18

E--> 301 <210> ~~SEQ ID NO. 15~~

302 <211> LENGTH: 29

303 <212> TYPE: DNA

304 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

```

306 <220> FEATURE:
307 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Eco RI
308 site
OK-> 310 <400> SEQUENCE: 15
311 gccgaattca gattgagcaa gagtataac 29
E--> 314 <210> SEQ ID NO. 16
315 <211> LENGTH: 19
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial
319 <220> FEATURE:
OK-> 320 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
OK-> 322 <400> SEQUENCE: 16
323 acctttataa agaccactc 19
E--> 326 <210> SEQ ID NO. 17
327 <211> LENGTH: 19
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial
331 <220> FEATURE:
OK-> 332 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
OK-> 334 <400> SEQUENCE: 17
335 acgcaatggg gaattgtac 19
E--> 338 <210> SEQ ID NO. 18
339 <211> LENGTH: 24
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial
343 <220> FEATURE:
OK-> 344 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
OK-> 346 <400> SEQUENCE: 18
347 aattcagatc tcaataattg agag 24
E--> 350 <210> SEQ ID NO. 19
351 <211> LENGTH: 24
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial
355 <220> FEATURE:
OK-> 356 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
OK-> 358 <400> SEQUENCE: 19
359 gatcctctca attattgaga tctg 24
E--> 362 <210> SEQ ID NO. 20
363 <211> LENGTH: 30
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
OK-> 368 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
OK-> 370 <400> SEQUENCE: 20
371 gcgggatcca ccatgtctct tcaacaagta 30
E--> 374 <210> SEQ ID NO. 21
375 <211> LENGTH: 30
376 <212> TYPE: DNA
377 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING

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TIME: 08:16:21

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

379 <220> FEATURE:

380 <223> OTHER INFORMATION: Oligonucleotide having Sac I site

~~OK~~-> 382 <400> SEQUENCE: 21

383 gccgagctct tagaactcca accacttttg

30

E--> 386 <210> ~~SEQ ID NO. 22~~

387 <211> LENGTH: 27

388 <212> TYPE: DNA

389 <213> ORGANISM: Artificial

391 <220> FEATURE:

~~OK~~-> 392 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site

E--> 394 <400> SEQUENCE: 22

395 ggcggatccg tctccagtt gttcttc

27

E--> 398 ⑦

Delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/520,033

DATE: 01/10/2006

TIME: 08:16:22

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\01102006\J520033.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
 L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
 L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:52 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
 L:78 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:89 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
 L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
 L:146 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:155 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
 L:159 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:168 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
 L:172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:181 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
 L:185 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:194 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
 L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:206 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
 L:210 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
 L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
 L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:273 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
 L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
 L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:297 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
 L:301 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
 L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
 L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:334 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
 L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
 L:350 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:358 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
 L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:370 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
 L:374 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
 L:386 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
 L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
 L:398 M:254 E: No. of Bases conflict, this line has no nucleotides.